updated 2/27/03 VP

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File 155:MEDLINE(R)  1966-2003/Feb W4
       (c) format only 2003 The Dialog Corp.

      Set  Items  Description
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?e pasteurella haemolytica

Ref    Items    RT  Index-term
E1         3        PASTEURELLA --RADIATION EFFECTS --RE
E2        39        PASTEURELLA --ULTRASTRUCTURE --UL
E3       497     1 *PASTEURELLA HAEMOLYTICA
E4        35        PASTEURELLA HAEMOLYTICA --CHEMISTRY --CH
E5        73        PASTEURELLA HAEMOLYTICA --CLASSIFICATION --CL
E6         2        PASTEURELLA HAEMOLYTICA --CYTOLOGY --CY
E7        39        PASTEURELLA HAEMOLYTICA --DRUG EFFECTS --DE
E8        39        PASTEURELLA HAEMOLYTICA --ENZYMOLOGY --EN
E9        91        PASTEURELLA HAEMOLYTICA --GENETICS --GE
E10       30        PASTEURELLA HAEMOLYTICA --GROWTH AND DEVELOPME
E11      145        PASTEURELLA HAEMOLYTICA --IMMUNOLOGY --IM
E12       95        PASTEURELLA HAEMOLYTICA --ISOLATION AND PURIFI

          Enter P or PAGE for more
?p

Ref    Items    RT  Index-term
E13       44        PASTEURELLA HAEMOLYTICA --METABOLISM --ME
E14       74        PASTEURELLA HAEMOLYTICA --PATHOGENICITY --PY
E15       23        PASTEURELLA HAEMOLYTICA --PHYSIOLOGY --PH
E16        3        PASTEURELLA HAEMOLYTICA --RADIATION EFFECTS --
E17        8        PASTEURELLA HAEMOLYTICA --ULTRASTRUCTURE --UL
E18        1        PASTEURELLA HAEMOLYTICA --VIROLOGY --VI
E19     2924     4  PASTEURELLA INFECTIONS
E20       62        PASTEURELLA INFECTIONS --BLOOD --BL
E21        5        PASTEURELLA INFECTIONS --CEREBROSPINAL FLUID -
E22        1        PASTEURELLA INFECTIONS --CLASSIFICATION --CL
E23      304        PASTEURELLA INFECTIONS --COMPLICATIONS --CO
E24        1        PASTEURELLA INFECTIONS --CONGENITAL --CN

          Enter P or PAGE for more
?s e3-e18
             497  PASTEURELLA HAEMOLYTICA
              35  PASTEURELLA HAEMOLYTICA --CHEMISTRY --CH
              73  PASTEURELLA HAEMOLYTICA --CLASSIFICATION --CL
               2  PASTEURELLA HAEMOLYTICA --CYTOLOGY --CY
              39  PASTEURELLA HAEMOLYTICA --DRUG EFFECTS --DE
              39  PASTEURELLA HAEMOLYTICA --ENZYMOLOGY --EN
              91  PASTEURELLA HAEMOLYTICA --GENETICS --GE
              30  PASTEURELLA HAEMOLYTICA --GROWTH AND DEVELOPME
             145  PASTEURELLA HAEMOLYTICA --IMMUNOLOGY --IM
              95  PASTEURELLA HAEMOLYTICA --ISOLATION AND PURIFI
              44  PASTEURELLA HAEMOLYTICA --METABOLISM --ME
              74  PASTEURELLA HAEMOLYTICA --PATHOGENICITY --PY
              23  PASTEURELLA HAEMOLYTICA --PHYSIOLOGY --PH
               3  PASTEURELLA HAEMOLYTICA --RADIATION EFFECTS --
               8  PASTEURELLA HAEMOLYTICA --ULTRASTRUCTURE --UL
               1  PASTEURELLA HAEMOLYTICA --VIROLOGY --VI
      S1       497  E3-E18
?s e9
      S2        91  'PASTEURELLA HAEMOLYTICA --GENETICS --GE'
?e e3

Ref    Items Type  RT  Index-term
R1       497        1 *PASTEURELLA HAEMOLYTICA
R2         6   X    4  MANNHEIMIA HAEMOLYTICA
?s r1-r4
             497  PASTEURELLA HAEMOLYTICA
               6  MANNHEIMIA HAEMOLYTICA
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                0
      S3      503  R1-R4
?e r2

Ref    Items Type  RT  Index-term
R1         6         4 *MANNHEIMIA HAEMOLYTICA
R2         6    X       DC=B3.440.450.600.500.500. (MANNHEIMIA HAEMOLYTICA)
R3         6    X       DC=B3.660.250.550.500.500. (MANNHEIMIA HAEMOLYTICA)
R4       497    X    1  PASTEURELLA HAEMOLYTICA
R5        93    B    4  MANNHEIMIA
?ds

Set     Items   Description
S1        497   E3-E18
S2         91   'PASTEURELLA HAEMOLYTICA --GENETICS --GE'
S3        503   R1-R4
?t s2/6/all
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2/6/1
13583471 22168198 PMID: 12180887
Phenotypic characterisation of Australian sheep and cattle isolates of Mannheimia haemolytica, Mannheimia granulomatis and Mannheimia varigena.
Jan-Feb 2002

2/6/2
13135010 21950584 PMID: 11953404
Construction and characterization of an acapsular mutant of Mannheimia haemolytica A1.
May 2002

2/6/3
13077276 21589082 PMID: 11731159
A putative iron-regulated TonB-dependent receptor of Mannheimia (Pasteurella) haemolytica A1: possible mechanism for phase variation.
Jan 3 2002

2/6/4
13077264 21589086 PMID: 11731163
Phenotypic and genotypic characterization of Mannheimia (Pasteurella) haemolytica-like strains isolated from diseased animals in Denmark.
Jan 3 2002

2/6/5
12758277 21423641 PMID: 11532607
Molecular genetic analysis of virulence in Mannheimia (pasteurella) haemolytica.
Sep 1 2001

2/6/6
12750263 21617389 PMID: 11741868
Mosaic structure and molecular evolution of the leukotoxin operon (lktCABD) in Mannheimia (Pasteurella) haemolytica, Mannheimia glucosida, and Pasteurella trehalosi.
Jan 2002

2/6/7
12695052 21427789 PMID: 11535337
Bordetella bronchiseptica fimbrial protein-enhanced immunogenicity of a Mannheimia haemolytica leukotoxin fragment.
Sep 14 2001

2/6/8
11358778 21437628 PMID: 11553565
Use of operon fusions in Mannheimia haemolytica to identify environmental and cis-acting regulators of leukotoxin transcription.
Oct 2001

2/6/9
11349019 21415990 PMID: 11524163
Genetic analysis of virulence factors of Mannheimia (Pasteurella) haemolytica A1.
Oct 22 2001

2/6/10
11265447 21295097 PMID: 11401986
Analysis of the capsule biosynthetic locus of Mannheimia (Pasteurella) haemolytica A1 and proposal of a nomenclature system.
Jul 2001

2/6/11
11225972 21254301 PMID: 11355660
Pulmonary expression of tumor necrosis factor alpha, interleukin-1 beta, and interleukin-8 in the acute phase of bovine pneumonic pasteurellosis.
May 2001

2/6/12
11075054 21101823 PMID: 11157953
Sequence diversity and molecular evolution of the leukotoxin (lktA) gene in bovine and ovine strains of Mannheimia (Pasteurella) haemolytica.
Feb 2001

2/6/13
11007267 20557867 PMID: 11108470
Contig selection in physical mapping.
2000

2/6/14
10776076 20316014 PMID: 10858203
Inactivation of Pasteurella (Mannheimia) haemolytica leukotoxin causes partial attenuation of virulence in a calf challenge model.
Jul 2000

2/6/15
10709588 20243463 PMID: 10779715
FnrP interactions with the Pasteurella haemolytica leukotoxin promoter.
May 1 2000

2/6/16
10599348 20135556 PMID: 10673001
Occurrence and structure-function relationship of pentameric short sequence repeats in microbial genomes.
Nov-Dec 1999

2/6/17
10496975 20031092 PMID: 10566816
Use of a polymerase chain reaction method to detect the leukotoxin gene lktA in biogroup and biovariant isolates of Pasteurella haemolytica and P

trehalosi.
Nov 1999

2/6/18
10309965 99296599 PMID: 10368164
Cloning and characterization of the gene encoding Pasteurella haemolytica FnrP, a regulator of the Escherichia coli silent hemolysin sheA.
Jun 1999

2/6/19
10282750 99261662 PMID: 10331277
CRITICA: coding region identification tool invoking comparative analysis.
Apr 1999

2/6/20
10174602 99157094 PMID: 10037813
Characterization of a CACAG pentanucleotide repeat in Pasteurella haemolytica and its possible role in modulation of a novel type III restriction-modification system.
Mar 15 1999

2/6/21
10154892 99152574 PMID: 10028248
Taxonomic relationships of the [Pasteurella] haemolytica complex as evaluated by DNA-DNA hybridizations and 16S rRNA sequencing with proposal of Mannheimia haemolytica gen. nov., comb. nov., Mannheimia granulomatis comb. nov., Mannheimia glucosida sp. nov., Mannheimia ruminalis sp. nov. and Mannheimia varigena sp. nov.
Jan 1999

2/6/22
10133463 99107940 PMID: 9889223
Pulsed-field gel electrophoresis is more efficient than ribotyping and random amplified polymorphic DNA analysis in discrimination of Pasteurella haemolytica strains.
Feb 1999

2/6/23
10119665 99098704 PMID: 9884235
The Pasteurella haemolytica 35 kDa iron-regulated protein is an FbpA homologue.
Dec 1998

2/6/24
10069187 99043883 PMID: 9826333
Genetic and immunologic analyses of PlpE, a lipoprotein important in complement-mediated killing of Pasteurella haemolytica serotype 1.
Dec 1998

2/6/25
10024424 98452721 PMID: 9781461
Characterization of a Pasteurella haemolytica A1 mutant deficient in production of three membrane lipoproteins.
Oct 1998

2/6/26
09805284 98223084 PMID: 9563620
Rapid spread of a unique strain of Pasteurella haemolytica serotype 1

among transported calves.
Apr 1998

2/6/27
09754694 98186055 PMID: 9526860
Biovariants of isolates of Pasteurella from domestic and wild ruminants.
Jan 1998

2/6/28
09717855 98133983 PMID: 9466945
Construction of an isogenic leukotoxin deletion mutant of Pasteurella haemolytica serotype 1: characterization and virulence.
Jan 1998

2/6/29
09669833 98070718 PMID: 9405205
Characterization of the Pasteurella haemolytica transferrin receptor genes and the recombinant receptor proteins.
Nov 1997

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09594173 98027314 PMID: 9361380
Genotypic relationships among strains classified under the (Pasteurella) haemolytica-complex as indicated by ribotyping and multilocus enzyme electrophoresis.
Oct 1997

2/6/31
09594172 98027313 PMID: 9361379
Further studies of the relationships among strains classified as taxon 15, taxon 18, taxon 20, (Pasteurella) granulomatis or the (Pasteurella) haemolytica-complex in ruminants using quantitative evaluation of phenotypic data.
Oct 1997

2/6/32
09531665 97427995 PMID: 9284183
A putative leucine zipper activator of Pasteurella haemolytica leukotoxin transcription and the potential for modulation of its synthesis by slipped-strand mispairing.
Sep 1997

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09531605 97427935 PMID: 9284123
Evolutionary genetics of Pasteurella haemolytica isolates recovered from cattle and sheep.
Sep 1997

2/6/34
09440837 97342728 PMID: 9199425
Generation of targeted nonpolar gene insertions and operon fusions in Pasteurella haemolytica and creation of a strain that produces and secretes inactive leukotoxin.
Jul 1997

2/6/35
09323665 97228420 PMID: 9074498
Plasmids for heterologous expression in Pasteurella haemolytica.

Feb 28 1997

2/6/36
09323664 97228419 PMID: 9074497
Cloning and characterization of the exbB-exbD-tonB locus of Pasteurella haemolytica A1.
Feb 28 1997

2/6/37
09292819 97189574 PMID: 9037761
Comparison of the recombinant and authentic forms of the Pasteurella haemolytica A1 glycoprotease.
Feb 1 1997

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09268369 97164347 PMID: 9011038
Isolation and characterization of the integration host factor genes of Pasteurella haemolytica.
Jan 15 1997

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09206476 97113561 PMID: 8955421
Rapid identification and cloning of bacterial transferrin and lactoferrin receptor protein genes.
Dec 1996

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09171259 97080552 PMID: 8921897
The restriction-modification system of Pasteurella haemolytica is a member of a new family of type I enzymes.
Oct 31 1996

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09158989 97051597 PMID: 8896274
The sequence of a 20.3 kb DNA fragment from the left arm of Saccharomyces cerevisiae chromosome IV contains the KIN28, MSS2, PHO2, POL3 and DUN1 genes, and six new open reading frames.
Sep 1996

2/6/42
09124283 97023877 PMID: 8870198
The isolation of recombinant plasmids expressing secreted antigens of Pasteurella haemolytica A1 and the characterization of an immunogenic 60 kDa antigen.
Aug 1996

2/6/43
09124279 97023873 PMID: 8870194
Genetic and immunological analyses of a 38 kDa surface-exposed lipoprotein of Pasteurella haemolytica A1.
Aug 1996

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09066188 96425875 PMID: 8828217
Characterization of epitopes involved in the neutralization of Pasteurella haemolytica serotype A1 leukotoxin.
Sep 1996

2/6/45
09018180 96376821 PMID: 8782683
Phylogenetic relationships and diversity within the Pasteurella haemolytica complex based on 16S rRNA sequence comparison and outer membrane protein and lipopolysaccharide analysis.
Jul 1996

2/6/46
08979551 96338388 PMID: 8726040
Distribution of tet(H) among Pasteurella isolates from the United States and Canada.
Jun 1996

2/6/47
08972709 96327137 PMID: 8759785
Occurrence of [copper, zinc]-cofactored superoxide dismutase in Pasteurella haemolytica and its serotype distribution.
Aug 15 1996

2/6/48
08965774 96333343 PMID: 8757837
Escherichia coli hemolysin mutants with altered target cell specificity.
Aug 1996

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08942325 96303514 PMID: 8757738
Binding-protein-dependent arginine transport in Pasteurella haemolytica.
Jul 1996

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08933729 96294781 PMID: 8698496
Pasteurella haemolytica leukotoxin induces bovine leukocytes to undergo morphologic changes consistent with apoptosis in vitro.
Jul 1996

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08861974 96227087 PMID: 8626262
Tetracycline resistance determinants, Tet B and Tet M, detected in Pasteurella haemolytica and Pasteurella multocida from bovine herds.
Nov 1995

2/6/52
08856157 96186484 PMID: 8641792
Cloning and characterization of the galE locus of Pasteurella haemolytica A1.
Mar 1996

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08824617 96176970 PMID: 8602834
The Pasteurella haemolytica O-sialoglycoprotein endopeptidase is inhibited by zinc ions and does not cleave fetuin.
Mar 7 1996

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08745587 96118702 PMID: 7496533
Functional analysis of the Bacillus subtilis purT gene encoding formate-dependent glycinamide ribonucleotide transformylase.

Sep 1995

2/6/55
08713031 96063020 PMID: 7579583
Sequence analysis of leukotoxin secretion determinants from a Pasteurella haemolytica-like organism.
1995

2/6/56
08675412 96021586 PMID: 7483245
Partial characterization of the leukotoxin of Pasteurella haemolytica-like bacteria isolated from swine enteritis.
Aug 1995

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08596566 95354962 PMID: 7628722
Construction of Actinobacillus pleuropneumoniae-Escherichia coli shuttle vectors: expression of antibiotic-resistance genes.
Jul 4 1995

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08553133 95309392 PMID: 7789505
Structural analysis and comparison of the C-terminal transport signal domains of hemolysin A and leukotoxin A.
Jun 5 1995

2/6/59
08542095 95301198 PMID: 7781993
Cloning and characterization of a gene from Pasteurella haemolytica A1 involved in lipopolysaccharide biosynthesis.
Jun 1 1995

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08526176 95281854 PMID: 7761696
A native plasmid of Pasteurella haemolytica serotype A1: DNA sequence analysis and investigation of its potential as a vector.
Mar 1995

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08448762 95197258 PMID: 7890392
Pasteurella haemolytica serotype 2 contains the gene for a noncapsular serotype 1-specific antigen.
Apr 1995

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08442991 95214513 PMID: 7700132
Expression, purification and immunologic analysis of three Pasteurella haemolytica A1 28-30 kDa lipoproteins.
Sep 1994

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08423227 95172695 PMID: 7868223
Isolation of Pasteurella haemolytica leukotoxin mutants.
Mar 1995

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08379584 95141537 PMID: 7839583

Construction and vaccine potential of an aroA mutant of Pasteurella haemolytica.
Sep 1994

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08254616 95011639 PMID: 7926822
Construction of isogenic mutants of Pasteurella haemolytica by allelic replacement.
Oct 11 1994

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08254456 95011479 PMID: 7926671
The detection of the sialoglycoprotease gene and assay for sialoglycoprotease activity among isolates of Pasteurella haemolytica A1 strains, serotypes A13, A14, T15 and A16.
Aug 15 1994

2/6/67
08227129 94361385 PMID: 8080187
A leukotoxin nonproducing mutant of Pasteurella haemolytica. Phagocytosis and killing by bovine polymorphonucleocytes.
Aug 15 1994

2/6/68
08184229 94320791 PMID: 8045428
Construction of conjugative shuttle and suicide vectors for Pasteurella haemolytica and P. multocida.
Jul 22 1994

2/6/69
08170196 94304176 PMID: 8031095
Molecular gene cloning and nucleotide sequencing and construction of an aroA mutant of Pasteurella haemolytica serotype A1.
Jun 1994

2/6/70
08167058 94300707 PMID: 8028096
Fatal pneumonia following inoculation of healthy bighorn sheep with Pasteurella haemolytica from healthy domestic sheep.
Apr 1994

2/6/71
08093619 94235161 PMID: 8179822
Static DNA bending and protein interactions within the Pasteurella haemolytica leukotoxin promoter region: development of an activation model for leukotoxin transcriptional control.
Feb 1994

2/6/72
08065374 94200580 PMID: 8150268
Preparation of recombinant glycoprotease of Pasteurella haemolytica A1 utilizing the Escherichia coli alpha-hemolysin secretion system.
Feb 15 1994

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07905050 94041617 PMID: 8225575
Molecular analysis of the leukotoxin determinants from Pasteurella haemolytica serotypes 1 to 16.

Dec 1993

2/6/74
07898277 94033621 PMID: 8219279
Cloning, sequencing and expression of a Pasteurella haemolytica A1 gene encoding a PurK-like protein.
1993

2/6/75
07875661 94013379 PMID: 7691872
Restriction endonuclease analysis and ribotyping differentiate Pasteurella haemolytica serotype A1 isolates from cattle within a feedlot.
Sep 1993

2/6/76
07873800 94011378 PMID: 8406866
Three contiguous lipoprotein genes in Pasteurella haemolytica A1 which are homologous to a lipoprotein gene in Haemophilus influenzae type b.
Nov 1993

2/6/77
07836493 93366458 PMID: 8359916
Expression of the Pasteurella haemolytica leukotoxin is inhibited by a locus that encodes an ATP-binding cassette homolog.
Sep 1993

2/6/78
07803580 93328110 PMID: 8335249
Analysis of tandem, multiple genes encoding 30-kDa membrane proteins in Pasteurella haemolytica A1.
Jul 15 1993

2/6/79
07724449 93248259 PMID: 8483936
Functional replacement of the hemolysin A transport signal by a different primary sequence.
May 1 1993

2/6/80
07693761 93216908 PMID: 8385150
Use of DNA analysis of Pasteurella haemolytica biotype T isolates to monitor transmission in bighorn sheep (Ovis canadensis canadensis).
Apr 1993

2/6/81
07690130 93212476 PMID: 8460470
Further characterization of Pasteurella haemolytica-like bacteria isolated from swine enteritis.
Mar 1993

2/6/82
07595934 93122524 PMID: 1478451
An analysis of the codon usage of Pasteurella haemolytica A1.
Dec 15 1992

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07566286 93091250 PMID: 1333838

Characterization of plasmids with antimicrobial resistant genes in Pasteurella haemolytica A1.
1992

2/6/84
07552809 93079434 PMID: 1448612
Construction of a broad host range shuttle vector for gene cloning and expression in Actinobacillus pleuropneumoniae and other Pasteurellaceae.
Mar-Apr 1992

2/6/85
07466856 92407490 PMID: 1527493
Distinct plasmid profiles of Pasteurella haemolytica serotypes and the characterization and amplification in Escherichia coli of ampicillin-resistance plasmids encoding ROB-1 beta-lactamase.
Jun 1992

2/6/86
07448699 92381834 PMID: 1324994
Using ribosomal RNA gene restriction patterns in distinguishing isolates of Pasteurella haemolytica from bighorn sheep (Ovis canadensis).
Jul 1992

2/6/87
07325520 92278215 PMID: 1816491
In vivo expression of iron regulated outer-membrane proteins in Pasteurella haemolytica-A1.
Nov 1991

2/6/88
07217071 92161482 PMID: 1789515
Characterization and comparison of antimicrobial susceptibilities and outer membrane protein and plasmid DNA profiles of Pasteurella haemolytica and certain other members of the genus Pasteurella.
Dec 1991

2/6/89
07216489 92160404 PMID: 1789017
Genomic distribution of a serotype 1-specific antigen-coding DNA fragment of Pasteurella haemolytica.
Oct 1991

2/6/90
07215876 92159547 PMID: 1788485
Occurrence and diversity of plasmids in ovine isolates of Pasteurella haemolytica.
Sep 1991

2/6/91
07191627 92104975 PMID: 1729215
Separable domains define target cell specificities of an RTX hemolysin from Actinobacillus pleuropneumoniae.
Jan 1992
?logoff hold
26feb03 11:01:36 User228206 Session D1924.2
$2.79 0.873 DialUnits File155
$0.00 91 Type(s) in Format 6
$0.00 91 Types
$2.79 Estimated cost File155

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      $0.46  TELNET
      $3.25  Estimated cost this search
      $3.25  Estimated total session cost   1.034 DialUnits


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### Status: Path 1 of [Dialog Information Services via Modem]

### Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
Trying 31060000009999...Open

DIALOG INFORMATION SERVICES
PLEASE LOGON:
 ******** HHHHHHHH SSSSSSSS?
### Status: Signing onto Dialog
 ********
ENTER PASSWORD:
 ******** HHHHHHHH SSSSSSSS? ********
Welcome to DIALOG
### Status: Connected


Dialog level 02.12.60D

Reconnected in file 155 26feb03 11:12:20
* *  New CURRENT Year ranges installed    **

File 155:MEDLINE(R)  1966-2003/Feb W4
       (c) format only 2003 The Dialog Corp.

      Set  Items  Description
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Cost is in DialUnits
?ds

Set     Items   Description
S1        497   E3-E18
S2         91   'PASTEURELLA HAEMOLYTICA --GENETICS --GE'
S3        503   R1-R4
?t s2/9/98 6 5 4 45 33 34 31 30 28 22 13 12 9 75 72 70 68 67 63 48 21 19 17 14

 2/9/98
>>>Item 98 is not within valid item range
?logoff hold
       26feb03 11:12:21 User228206 Session D1924.3
            $0.48    0.149 DialUnits File155
     $0.48  Estimated cost File155
     $0.22  TELNET
     $0.70  Estimated cost this search
     $0.70  Estimated total session cost   0.149 DialUnits


### Status: Signed Off. (1 minutes)

### Status: Path 1 of [Dialog Information Services via Modem]

### Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
Trying 31060000009999...Open

DIALOG INFORMATION SERVICES
PLEASE LOGON:
 ******** HHHHHHHH SSSSSSSS?
### Status: Signing onto Dialog
 ********
```

ENTER PASSWORD:
******** HHHHHHHH SSSSSSSS? ********
Welcome to DIALOG
Status: Connected

Dialog level 02.12.60D

Reconnected in file 155 26feb03 11:13:02
* * New CURRENT Year ranges installed **

File 155:MEDLINE(R) 1966-2003/Feb W4
(c) format only 2003 The Dialog Corp.

Set Items Description
--- ----- -----------
Cost is in DialUnits
?ds

Set Items Description
S1 497 E3-E18
S2 91 'PASTEURELLA HAEMOLYTICA --GENETICS --GE'
S3 503 R1-R4
?t s2/9/89 6 5 4 45 33 34 31 30 28 22 13 12 9 75 72 70 68 67 63 48 21 19 17 14

2/9/89
DIALOG(R)File 155:MEDLINE(R)

07216489 92160404 PMID: 1789017
Genomic distribution of a serotype 1-specific antigen-coding DNA fragment of Pasteurella haemolytica.
Gonzalez C; Murtaugh M P; Maheswaran S K
Department of Veterinary Pathobiology, University of Minnesota, St. Paul 55108.
Zentralblatt fur Veterinarmedizin. Reihe B. Journal of veterinary medicine. Series B (GERMANY) Oct 1991, 38 (8) p599-609, ISSN 0514-7166 Journal Code: 0331325
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
A genomic fragment of Pasteurella haemolytica biotype A coding for a serotype 1-specific agglutinating antigen was used as a probe in a series of hybridization experiments to determine distribution of the fragment in various P. haemolytica serotypes as well as other bacteria. Results showed presence of the fragment in seven out of the 12 serotypes tested, all of which belonged to biotype A. Two other serotypes belonging to biotype A, all three serotypes belonging to biotype T, two Pasteurella multocida isolates and Escherichia coli did not have the fragment in their genome. Thus the expression of the P. haemolytica biotype A serotype 1-specific agglutinating antigen (PHA1SAA) seems to be due to serotype-specific regulation of protein expression rather than to genetic deletion. Differences in methylation of the PHA1SAA-coding fragment was also noted in DpnI and Sau3AI genomic DNA digests from the various serotypes analyzed by Southern blot. However, no apparent correlation was observed between methylation and PHA1SAA expression. E. coli with a recombinant plasmid containing a homologous genomic fragment derived from P. haemolytica serotype 2 also expressed PHA1SAA.
Tags: Animal; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.
Descriptors: Antigens, Bacterial--genetics--GE; *DNA, Bacterial--genetics --GE; * **Pasteurella haemolytica** --genetics--GE; Cattle; Cloning, Molecular; DNA Probes; Gene Expression Regulation, Bacterial; Nucleic Acid Hybridization
CAS Registry No.: 0 (Antigens, Bacterial); 0 (DNA Probes); 0 (DNA, Bacterial)

13077264 21589086 PMID: 11731163

Phenotypic and genotypic characterization of Mannheimia (Pasteurella) haemolytica-like strains isolated from diseased animals in Denmark.

Angen Oystein; Ahrens Peter; Bisgaard Magne

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Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Trehalose-negative strains of the Pasteurella haemolytica complex have recently been transferred to a new genus, Mannheimia. This genus presently consists of five named species: M. haemolytica, M. glucosida, M. granulomatis, M. ruminalis and M. varigena. The purpose of this study was to investigate the occurrence of these species and lesions associated with these isolates in Denmark. In all 106 M. haemolytica-like strains isolated from pathological material from cattle, sheep, pigs and hares submitted to the Danish Veterinary Laboratory between 1994 and 1998 were investigated. Phenotypic characterization and ribotyping were used for identification in addition to sequencing of the 16S rRNA genes for selected strains. The species allocation was determined by comparison to results from a previous polyphasic taxonomic study. Seventy-one percent of the strains belonged to M. haemolytica, 18% to M. varigena and 8% to unnamed groups within the genus Mannheimia. Single isolates identified as M. glucosida and P. trehalosi, respectively, were detected. Two isolates belonged to M. granulomatis. Forty-three percent of the strains belonged to serotype 1, 41% were untypeable, while the rest belonged to serotypes 2, 7, 9, and 16. The present investigation also showed that a simplified phenotypic characterization using Diatabs Diagnostic Tablets (Rosco, Denmark) represents a useful method for obtaining a quick and reliable species identification. Finally, the investigation confirmed that serotyping does not represent a reliable method for species identification. The heterogeneity of species associated with bovine "pasteurellosis" should be considered in future studies to improve our understanding of the pathogenesis of pneumonic disease.

Tags: Animal

Descriptors: *DNA, Bacterial--chemistry--CH; *Pasteurella Infections --veterinary--VE; *Pasteurella haemolytica--classification--CL; *RNA, Ribosomal, 16S--genetics--GE; *Respiratory Tract Diseases--veterinary--VE; Cattle; DNA, Bacterial--analysis--AN; Denmark; Genotype; Lagomorpha; Pasteurella Infections--diagnosis--DI; Pasteurella Infections --microbiology--MI; **Pasteurella haemolytica** --genetics--GE; Phenotype; Phylogeny; RNA, Ribosomal, 16S--analysis--AN; Respiratory Tract Diseases --diagnosis--DI; Respiratory Tract Diseases--microbiology--MI; Ribotyping --veterinary--VE; Sheep; Swine

CAS Registry No.: 0 (DNA, Bacterial); 0 (RNA, Ribosomal, 16S)

Record Date Created: 20011203

2/9/45

09018180 96376821 PMID: 8782683

Phylogenetic relationships and diversity within the Pasteurella haemolytica complex based on 16S rRNA sequence comparison and outer membrane protein and lipopolysaccharide analysis.

Davies R L; Paster B J; Dewhirst F E

Division of Infection and Immunity, University of Glasgow, Scotland, United Kingdom.

International journal of systematic bacteriology (UNITED STATES) Jul 1996, 46 (3) p736-44, ISSN 0020-7713 Journal Code: 0042143

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The outer membrane protein (OMP) and lipopolysaccharide (LPS) profiles of 30 untypeable isolates of Pasteurella haemolytica were examined by sodium dodecyl sulfate-polyacrylamide gel electrophoresis and compared with the profiles of typeable isolates. The phylogenetic relationships of 28 isolates representing each of the serotypes of P. haemolytica and Pasteurella trehalosi, as well as untypeable isolates of P. haemolytica, were determined by comparing 16S rRNA sequences. The analysis of the OMP and LPS profiles of the untypeable isolates revealed five groups, which were designated untypeable groups 1 (UG1) through UG5. The UG1 and UG2 isolates had OMP and LPS profiles identical to the profiles of certain serotype A1 and A2 isolates, respectively. Furthermore, UG1 isolates originating from cattle and sheep could be clearly differentiated on the basis of their OMP profiles. The OMP and LPS profiles of UG3 isolates were similar appearance to the profiles of serotype A11 isolates, suggesting that these two groups are closely related. The OMP profiles of UG4 and UG5 isolates were unique and different from the OMP profiles of the UG1 through UG3 isolates. A comparison of 16S rRNA sequences revealed that typeable isolates of P. haemolytica could be divided into the following three groups: (i) serotype A1, A5 through A9, A12 through A14, and A16 isolates, (ii) serotype A2 isolates, and (iii) serotype A11 isolates. the isolates belonging to the first group all had identical sequences, whereas the sequences of isolates belonging to the second and third groups differed from the sequences of the isolates belonging to the first group at two and four base positions, respectively. The sequence data for the untypeable isolates confirmed the conclusions derived from the OMP and LPS analysis. Isolates belonging to UG1 and UG2 were identical to serotype A1 and A2 isolates, respectively; isolates belonging to UG3 were related to serotype A11 isolates, although there was some sequence heterogeneity within this group; and isolates belonging to UG4 and UG5 were more distantly related to P. haemolytica than were isolates belonging to UG1 through UG3 and were clearly members of two different species. As expected, isolates of P. trehalosi were event more distantly related to P. haemolytica than were the untypeable isolates, but there was significantly more sequence variation among the four serotypes of this species than there was among the serotypes of P. haemolytica. The correlation of the OMP and LPS data with the 16S rRNA sequence data suggested that OMP and LPS analyses might be useful for preliminary screening and comparing large numbers of isolates in taxonomic and epidemiological studies of the Pasteurellaceae.

Tags: Animal; Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Pasteurella haemolytica--classification--CL; Bacterial Outer Membrane Proteins--analysis--AN; Base Sequence; Cattle; DNA, Bacterial; Lipopolysaccharides--analysis--AN; Molecular Sequence Data; **Pasteurella haemolytica** --genetics--GE; Pasteurella haemolytica --metabolism--ME; Phylogeny; RNA, Bacterial; RNA, Ribosomal, 16S; Sheep; Variation (Genetics)

Molecular Sequence Databank No.: GENBANK/M75062; GENBANK/M75063; GENBANK/M75065; GENBANK/M75066; GENBANK/U57066; GENBANK/U57067; GENBANK/U57068; GENBANK/U57069; GENBANK/U57070; GENBANK/U57071; GENBANK/U57072; GENBANK/U57073; GENBANK/U57074; GENBANK/U57075; GENBANK/U57076; GENBANK/U57077; GENBANK/U57078

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (DNA, Bacterial); 0 (Lipopolysaccharides); 0 (RNA, Bacterial); 0 (RNA, Ribosomal, 16S)

Record Date Created: 19961021

2/9/33

09531605 97427935 PMID: 9284123

Evolutionary genetics of Pasteurella haemolytica isolates recovered from cattle and sheep.

Davies R L; Arkinsaw S; Selander R K

Department of Microbiology and Immunology, Baylor College of Medicine, Houston, Texas 77030, USA.
Infection and immunity (UNITED STATES) Jul 1997, 65 (7) p2593-8, ISSN 0019-9567 Journal Code: 0246127
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
An efficient method for targeted gene inactivation and generation of chromosomal gene fusions in Pasteurella haemolytica has been devised and used to create an lktC::cat operon fusion by allelic exchange at the leukotoxin gene cluster (lktCABD). A copy of the lktC gene was insertionally inactivated by using a nonpolar, promoterless cat cassette and then delivered into P. haemolytica on a shuttle vector. Plasmid incompatibility was used to detect clones where double recombination events had occurred at the chromosomal locus. The insertion in lktC did not affect expression of the downstream genes, and the mutant strain secreted an antigenic proleukotoxin that was neither leukotoxic nor hemolytic. Expression of the lktC gene in trans restored the wild-type phenotype, confirming that LktC is required for activation of the proleukotoxin to the mature leukotoxin. Construction of the lktC::cat operon fusion allowed us to quantitate leukotoxin promoter activity in P. haemolytica and to demonstrate that transcription was maximal during early logarithmic growth phase but was reduced following entry into late logarithmic phase. This allelic exchange system should be useful for future genetic studies in P. haemolytica and could potentially be applied to other members of Haemophilus-Actinobacillus-Pasteurella family, where genetic manipulation is limited.
Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.
Descriptors: Bacterial Toxins--genetics--GE; *Cytotoxins--genetics--GE; *Exotoxins--genetics--GE; *Operon; * **Pasteurella haemolytica** --genetics--GE ; Bacterial Toxins--metabolism--ME; Cloning, Molecular; Cytotoxins --metabolism--ME; Exotoxins--metabolism--ME; Genetic Vectors; Transcription, Genetic
CAS Registry No.: 0 (Bacterial Toxins); 0 (Cytotoxins); 0 (Exotoxins); 0 (Genetic Vectors); 0 (leukotoxin)
Record Date Created: 19970721

2/9/31

09594172 98027313 PMID: 9361379

Further studies of the relationships among strains classified as taxon 15, taxon 18, taxon 20, (Pasteurella) granulomatis or the (Pasteurella) haemolytica-complex in ruminants using quantitative evaluation of phenotypic data.

Angen O; Olsen J E; Bisgaard M
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Zentralblatt fur Bakteriologie : international journal of medical microbiology (GERMANY) Oct 1997, 286 (3) p317-32, ISSN 0934-8840 Journal Code: 9203851
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Ninety-three trehalose-negative (P.) haemolytica-like strains of ruminant, porcine and leprine origin were investigated. A quantitative evaluation of phenotypic tests was used and the results obtained were compared with those from 246 previously investigated ruminant strains. Cluster analysis of the results obtained displayed most of the taxa as distinct groups which could be related to differences in key characters. Although only minor phenotypic differences were observed between the taxa

investigated and the taxa were internally heterogeneous for m of the tests, it was possible to identify characters separating most groups. However, in three instances, taxa isolated from different species could not be separated by any of the tests used or by quantitative evaluation of all 79 tests--the only difference being the species of animals from which they had been isolated. Taxa which could not be separated by phenotypic tests included the ruminant biogroup 6 of (P.) haemolytica and the porcine taxon 15/biovar 1, the ruminant biogroup 7 of (P.) haemolytica and the porcine taxon 15/biovar 2, and ruminant biogroup 31 of (P.) haemolytica and the leprine taxon 20/biovar 1.

Tags: Animal; Support, Non-U.S. Gov't

Descriptors: *Pasteurella--classification--CL; *Pasteurella haemolytica --classification--CL; Bacteriological Techniques; Classification; Culture Media--metabolism--ME; Pasteurella--genetics--GE; Pasteurella--metabolism --ME; **Pasteurella haemolytica** --genetics--GE; Pasteurella haemolytica --metabolism--ME; Phylogeny; Rabbits; Rumen--microbiology--MI; Ruminants; Swine

CAS Registry No.: 0 (Culture Media)

Record Date Created: 19971215

2/9/30

DIALOG(R)File 155:MEDLINE(R)

09594173 98027314 PMID: 9361380

Genotypic relationships among strains classified under the (Pasteurella) haemolytica-complex as indicated by ribotyping and multilocus enzyme electrophoresis.

Angen O; Caugant D A; Olsen J E; Bisgaard M

Department of Veterinary Microbiology, Royal Veterinary and Agricultural University, Frederiksberg C, Denmark. ang@svs.dk

Zentralblatt fur Bakteriologie : international journal of medical microbiology (GERMANY) Oct 1997, 286 (3) p333-54, ISSN 0934-8840

Journal Code: 9203851

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Two-hundred and one strains classified under the (Pasteurella) haemolytica-complex isolated from cattle, sheep, deer, pigs, hares and rabbits were investigated by ribotyping. Fifty-nine of these strains were selected for further studies using multilocus enzyme electrophoresis (MEE). A correlation between the clusters identified by ribotyping and MEE was demonstrated and the results furthermore indicated that a genetic basis exists for most clusters previously outlined by the use of quantitative evaluation of phenotypic data. The taxonomic relevance of ornithine decarboxylase and fermentation of L-arabinose, D-sorbitol and glucosides for taxonomic delineation within the (P.) haemolytica-complex was supported. A taxonomic importance was further indicated for ONPG, ONPX, ONPF, meso-inositol, D-xylose, maltose, dextrine and NPG in relation to some of the taxa. Within the porcine taxon 15, however, differences in ornithine decarboxylase did not correspond to genetic clusters. Six lineages were revealed by MEE. Lineage A contained electrophoretic types (ETs) representing biogroups 1, 3A-3H, 8A and 9, indicating a genetic relationship between these groups--an observation which was supported by ribotyping. Lineage B included biogroup 8D, 3 strains from biogroup 10 and a single strain from biogroup 1 and taxon 18/biovar 1. Lineage C contained strains allocated to biogroup 6 from ruminants and the porcine taxon 15. The similarity between these two groups was accentuated by ribotyping. Lineage D and the single isolate in lineage E contained strains allocated to biogroups 7, 10, 8B and 8C, in addition to single strains from biogroups 6 and 9. The same strains were found in the heterogenous ribotype cluster 17. Lineage F contained strains representing the leprine taxon 20 and the ruminant (P.) granulomatis. Ribotyping indicated that the ruminant biogroup 3J was affiliated with both taxon 20 and (P.) granulomatis.

Tags: Animal; Support, Non-U.S. Gov't

Descriptors: *DNA, Bacterial--analysis--AN; *Enzymes--analysis--AN; *Pasteurella haemolytica--classification--CL; *RNA, Ribosomal, 16S --genetics--GE; *RNA, Ribosomal, 23S--genetics--GE; Alleles; Arabinose --metabolism--ME; Cattle; Deer; Glucosides--metabolism--ME; Inositol --metabolism--ME; Nucleic Acid Hybridization; Ornithine Decarboxylase --genetics--GE; Pasteurella haemolytica--enzymology--EN; **Pasteurella haemolytica** --genetics--GE; Phylogeny; Rabbits; Sheep; Sorbitol--metabolism --ME; Swine; Xylose--metabolism--ME; Xylosidases--metabolism--ME; alpha-L-Fucosidase--metabolism--ME; beta-Galactosidase--metabolism--ME

CAS Registry No.: 0 (DNA, Bacterial); 0 (Enzymes); 0 (Glucosides); 0 (RNA, Ribosomal, 16S); 0 (RNA, Ribosomal, 23S); 0 (Xylose); 147-81-9 (Arabinose); 50-70-4 (Sorbitol); 6917-35-7 (Inositol)

Enzyme No.: EC 3.2.1.- (Xylosidases); EC 3.2.1.23 (beta-Galactosidase); EC 3.2.1.37 (exo-1,4-beta-D-xylosidase); EC 3.2.1.51 (alpha-L-Fucosidase); EC 4.1.1.17 (Ornithine Decarboxylase)

Record Date Created: 19971215

2/9/28

DIALOG(R)File 155:MEDLINE(R)

09717855 98133983 PMID: 9466945

Construction of an isogenic leukotoxin deletion mutant of Pasteurella haemolytica serotype 1: characterization and virulence.

Tatum F M; Briggs R E; Sreevatsan S S; Zehr E S; Ling Hsuan S; Whiteley L O; Ames T R; Maheswaran S K

National Animal Disease Center, U.S. Department of Agriculture, Ames, IA 50010, USA.

Microbial pathogenesis (ENGLAND) Jan 1998, 24 (1) p37-46, ISSN 0882-4010 Journal Code: 8606191

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Allelic replacement was used to generate two isogenic lktA deletion mutants of Pasteurella haemolytica serotype 1 that were incapable of synthesizing leukotoxin (Lkt). Southern blot data confirmed that lktA sequences were absent in the two P. haemolytica deletion mutants. Culture supernatants and whole cell lysates from the wild type P. haemolytica, D153 parent strain, but not the lktA deletion mutants, contained immunoreactive and bioactive leukotoxic protein. In addition, only the parent strain was haemolytic when grown on bovine and sheep blood agar plates. Virulence of the lktA deletion mutant, lktA 77, was compared with the parent in an experimentally infected calf model of pneumonic pasteurellosis. Results revealed significant reduction in virulence in the lktA mutant as measured by clinical and lung lesion scores. Notable differences in histological changes such as markedly reduced necrosis and lack of leukocyte degeneration occurred in calves infected with the lktA mutant in comparison with those infected with the parent wild-type strain. Thus, it appears that leukotoxin plays a important role in the pathogenesis of lung injury in bovine pneumonic pasteurellosis. Copyright 1998 Academic Press Limited.

Tags: Animal; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Descriptors: Exotoxins--genetics--GE; *Gene Deletion; *Genes, Bacterial; *Hemolysins--genetics--GE; * **Pasteurella haemolytica** --genetics--GE; *Pasteurella haemolytica--pathogenicity--PY; Base Sequence; Cattle; DNA Primers--genetics--GE; Exotoxins--physiology--PH; Hemolysins--physiology --PH; Lung--pathology--PA; Pasteurella haemolytica--classification--CL; Pasteurellosis, Pneumonic--etiology--ET; Pasteurellosis, Pneumonic --pathology--PA; Serotyping; Virulence--genetics--GE; Virulence --physiology--PH

CAS Registry No.: 0 (DNA Primers); 0 (Exotoxins); 0 (Hemolysins); 0 (leukotoxin A)

Record Date Created: 19980324

2/9/22

DIALOG(R)File 155:MEDLINE(R)

10133463 99107940 PMID: 9889223

Pulsed-field gel electrophoresis is more efficient than ribotyping and random amplified polymorphic DNA analysis in discrimination of Pasteurella haemolytica strains.

Kodjo A; Villard L; Bizet C; Martel J L; Sanchis R; Borges E; Gauthier D; Maurin F; Richard Y

Ecole Nationale Veterinaire de Lyon, F-69280 Marcy l'Etoile, France. a.kodjo@vet-lyon.fr

Journal of clinical microbiology (UNITED STATES) Feb 1999, 37 (2) p380-5, ISSN 0095-1137 Journal Code: 7505564

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

One hundred thirty-three strains of Pasteurella haemolytica of both biotypes (90 and 43 strains of biotypes A and T, respectively) and almost all the serotypes were subjected to ribotyping, random amplified polymorphic DNA (RAPD) analysis, and pulsed-field gel electrophoresis (PFGE) analysis for epidemiological purposes. A total of 15 patterns recorded as ribotypes HA to HO were found for the P. haemolytica biotype A strains, with ribotypes HA, HC, and HD being encountered most often (66 strains [74%]); and 20 ribotypes, designated HA' to HT', that were clearly distinct from those observed for biotype A strains were observed for strains of biotype T. RAPD analysis generated a total of 44 (designated Rp1 to Rp44) and 15 (designated Rp1' to Rp 15') unique RAPD patterns for biogroup A and biogroup T, respectively. Analysis of the data indicated that a given combined ribotype-RAPD pattern could be observed for biotype A strains of different serotypes, whatever the zoological or geographic origin, whereas this was not the case for biotype T strains. PFGE appeared to be more efficient in strain discrimination since selected strains from various zoological or geographical origins harboring the same ribotype-RAPD group were further separated into unique entities.

Tags: Animal; Comparative Study; Support, Non-U.S. Gov't

Descriptors: Bacterial Typing Techniques; *Electrophoresis, Gel, Pulsed-Field; *Pasteurella Infections--veterinary--VE; *Pasteurella haemolytica--classification--CL; * **Pasteurella haemolytica** --genetics--GE ; DNA, Bacterial--chemistry--CH; DNA, Ribosomal--chemistry--CH; Genes, rRNA ; Pasteurella Infections--epidemiology--EP; Pasteurella Infections --microbiology--MI; RNA, Ribosomal--genetics--GE; Random Amplified Polymorphic DNA Technique; Restriction Mapping

CAS Registry No.: 0 (DNA, Bacterial); 0 (DNA, Ribosomal); 0 (RNA, Ribosomal)

Record Date Created: 19990224

2/9/13

DIALOG(R)File 155:MEDLINE(R)

11007267 20557867 PMID: 11108470

Contig selection in physical mapping.

Heber S; Stoye J; Frohme M; Hoheisel J; Vingron M

German Cancer Research Center (DKFZ), Theoretical Bioinformatics (H0300), Heidelberg, Germany. s.heber@dkfz-heidelberg.de

Journal of computational biology : a journal of computational molecular cell biology (UNITED STATES) 2000, 7 (3-4) p395-408, ISSN 1066-5277 Journal Code: 9433358

Document type: Journal Article; Validation Studies

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

lineages of ovine serotype A2 strains possess lktA alleles that have very different evolutionary histories and encode divergent leukotoxins (5.3% amino acid divergence), but both contain segments derived from the bovine allele. Homologous segments of donor and recipient alleles are identical or nearly identical, indicating that the recombination events are relatively recent and probably postdate the domestication of cattle and sheep. Our findings suggest that host switching of bovine strains from cattle to sheep, together with inter- and intraspecies recombinational exchanges, has played an important role in generating leukotoxin diversity in ovine strains. In contrast, there is limited allelic diversity of lktA in bovine strains, suggesting that transmission of strains from sheep to cattle has been less important in leukotoxin evolution.

Tags: Animal; Comparative Study; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: Evolution, Molecular; *Exotoxins--genetics--GE; *Hemolysins --genetics--GE; * **Pasteurella haemolytica** --genetics--GE; *Pasteurellosis, Pneumonic--microbiology--MI; *Sheep Diseases--microbiology--MI; Alleles; Amino Acid Sequence; Cattle; Conserved Sequence; Models, Genetic; Molecular Sequence Data; Pasteurella haemolytica--classification--CL; Pasteurellosis, Pneumonic--genetics--GE; Recombination, Genetic; Serotyping; Sheep; Sheep Diseases--genetics--GE; Species Specificity; Variation (Genetics)

Molecular Sequence Databank No.: GENBANK/AF314503; GENBANK/AF314504; GENBANK/AF314505; GENBANK/AF314506; GENBANK/AF314507; GENBANK/AF314508; GENBANK/AF314509; GENBANK/AF314510; GENBANK/AF314511; GENBANK/AF314512; GENBANK/AF314513; GENBANK/AF314514; GENBANK/AF314515; GENBANK/AF314516; GENBANK/AF314517; GENBANK/AF314518; GENBANK/AF314519; GENBANK/AF314520; GENBANK/AF314521; GENBANK/AF314522; GENBANK/AF314523; GENBANK/AF314524; GENBANK/AF314525; GENBANK/AF314526

CAS Registry No.: 0 (Exotoxins); 0 (Hemolysins); 0 (leukotoxin A)

Record Date Created: 20010222

2/9/9

DIALOG(R)File 155:MEDLINE(R)

11349019 21415990 PMID: 11524163

Genetic analysis of virulence factors of Mannheimia (Pasteurella) haemolytica A1.

Lo R Y

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Veterinary microbiology (Netherlands) Oct 22 2001, 83 (1) p23-35, ISSN 0378-1135 Journal Code: 7705469

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Using a molecular genetic approach, the genes that code for the various virulence factors of Mannheimia haemolytica A1 have been cloned for detailed characterizations. These included analysis of the encoded proteins, their biological activities, secretion of the molecules from the bacterium as well as their use in a vaccine component.Two newly characterized antigens of M. haemolytica A1 have been identified. The first one is a TonB-dependent iron regulated outer-membrane receptor that is distinct from the transferrin binding proteins. The 84kDa Irp protein exhibits features including a TonB box and a 50 amino acid region that can adopt occluded beta-barrel structures similar to the "plug" domain of the Escherichia coli FhuA and FepA crystal structures. Homologues of Irp were identified by analysis of the genome sequences of a number of Gram negative mucosal pathogens, including Neisseria meningitidis and N. gonorrhoeae. The Neisserial irp genes were cloned by PCR and expressed the 84kDa protein as expected, demonstrating that they are functional genes. In addition to being regulated by iron and Fur, irp(Mh) undergoes phase variation by a slipped-strand mispairing mechanism and may represent a contingency locus for iron acquisition during an infection.Another locus that codes for a

putative adhesin molecule has also been partially characterized. This putative adhesin protein is highly homologous with the high-molecular-weight adhesin proteins of non-piliated non-typable strains of Haemophilus influenzae (NTHi) including Hia, Hsf, HMW1, HMW2. Currently, we have cloned the DNA that codes for 2223 amino acids (225kDa) and is still missing the stop codon. It is anticipated that when complete, the protein could be close to 240kDa, similar to the molecular mass of Hsf. Though incomplete, analysis of the adhesin showed that it exhibits characteristics of autotransporter (AT) proteins. The role of this high-molecular-weight adhesin in infection is being investigated. (39 Refs.)

Tags: Animal; Support, Non-U.S. Gov't

Descriptors: Adhesins, Bacterial--genetics--GE; *Bacterial Proteins --genetics--GE; * **Pasteurella haemolytica** --genetics--GE; *Pasteurella haemolytica--pathogenicity--PY; *Pasteurellosis, Pneumonic--microbiology --MI; Base Sequence; Blotting, Western; Cattle; Gene Expression Regulation, Bacterial; Molecular Weight; Virulence--genetics--GE

CAS Registry No.: 0 (Adhesins, Bacterial); 0 (Bacterial Proteins)

Record Date Created: 20010828

2/9/75

DIALOG(R)File 155:MEDLINE(R)

07875661 94013379 PMID: 7691872

Restriction endonuclease analysis and ribotyping differentiate Pasteurella haemolytica serotype A1 isolates from cattle within a feedlot.

Murphy G L; Robinson L C; Burrows G E

Department of Veterinary Pathology, College of Veterinary Medicine, Oklahoma State University, Stillwater 74078.

Journal of clinical microbiology (UNITED STATES) Sep 1993, 31 (9) p2303-8, ISSN 0095-1137 Journal Code: 7505564

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Pasteurella haemolytica serotype A1 isolates were collected from cattle within a feedlot during an outbreak of bovine respiratory disease. Genetic heterogeneity among the isolates was examined by restriction endonuclease analysis (REA), ribotyping, and analysis of plasmid content. The susceptibilities of isolates to several antibiotics were also examined. Five different REA patterns and three different ribotypes were observed among the isolates. Fifty percent of the isolates had an identical REA type, ribotype, and plasmid profile. Examination of the plasmid content of the isolates revealed that most (73%) carry a single plasmid which encodes beta-lactamase, 13.5% carry two plasmids, and 13.5% carry no plasmid. The data reveal the presence of genetic differences among isolates of P. haemolytica A1, associated with shipping fever pneumonia within a closed feedlot, and suggest that a combination of REA, ribotyping, plasmid analysis, and antibiotic susceptibility determination will be useful in analyzing the molecular epidemiology of this disease.

Tags: Animal; Support, Non-U.S. Gov't

Descriptors: DNA Restriction Enzymes; *DNA, Bacterial--analysis--AN; * **Pasteurella haemolytica** --genetics--GE; *Pasteurellosis, Pneumonic --microbiology--MI; *RNA, Ribosomal--genetics--GE; Bacterial Typing Techniques; Cattle; Drug Resistance, Microbial; Pasteurella haemolytica --classification--CL; Plasmids; Polymorphism, Restriction Fragment Length; RNA Probes; RNA, Bacterial--genetics--GE; Serotyping

CAS Registry No.: 0 (DNA, Bacterial); 0 (Plasmids); 0 (RNA Probes); 0 (RNA, Bacterial); 0 (RNA, Ribosomal)

Enzyme No.: EC 3.1.21 (DNA Restriction Enzymes)

Record Date Created: 19931102

2/9/72

DIALOG(R)File 155:MEDLINE(R)

08065374 94200580 PMID: 8150268

Preparation of recombinant glycoprotease of Pasteurella haemolytica A1 utilizing the Escherichia coli alpha-hemolysin secretion system.

Lo R Y; Watt M A; Gyroffy S; Mellors A
Department of Microbiology, University of Guelph, Ontario, Canada.

FEMS microbiology letters (NETHERLANDS) Feb 15 1994, 116 (2) p225-30 , ISSN 0378-1097 Journal Code: 7705721
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Three murine monoclonal antibodies were prepared against the recombinant glycoprotease of Pasteurella haemolytica A1 expressed in Escherichia coli. These monoclonal antibodies were able to recognize the authentic glycoprotease from P. haemolytica A1 culture supernatant. A recombinant plasmid which contained most of the glycoprotease gene of P. haemolytica A1 fused with the secretion signal sequence from hlyA of the E. coli alpha-hemolysin determinant was constructed. This recombinant plasmid expressed a fusion protein (Gcp-F) which was secreted into the culture supernatant by E. coli cells when the alpha-hemolysin secretion functions HlyB and HlyD are supplied in trans. Gcp-F could be readily recovered from the supernatant free from other cellular materials and is suitable for use in vaccine trials and challenge experiments in animals.

Tags: Support, Non-U.S. Gov't
Descriptors: *Genes, Bacterial--genetics--GE; *Metalloendopeptidases --biosynthesis--BI; *Pasteurella haemolytica--enzymology--EN; *Recombinant Fusion Proteins--biosynthesis--BI; Amino Acid Sequence; Antibodies, Bacterial; Antibodies, Monoclonal; Base Sequence; Endotoxins--analysis--AN; Gene Expression Regulation, Bacterial--genetics--GE; Hemolysins--genetics --GE; Metalloendopeptidases--genetics--GE; Metalloendopeptidases--immunolo gy--IM; Metalloendopeptidases--isolation and purification--IP; Metalloendopeptidases--secretion--SE; Molecular Sequence Data; **Pasteurella haemolytica** --genetics--GE; Plasmids; Protein Sorting Signals --genetics--GE; Recombinant Fusion Proteins--immunology--IM; Recombinant Fusion Proteins--isolation and purification--IP; Recombinant Fusion Proteins--secretion--SE
CAS Registry No.: 0 (Antibodies, Bacterial); 0 (Antibodies, Monoclonal); 0 (Endotoxins); 0 (Hemolysins); 0 (Plasmids); 0 (Protein Sorting Signals); 0 (Recombinant Fusion Proteins)
Enzyme No.: EC 3.4.24 (Metalloendopeptidases); EC 3.4.24.57 (O-sialoglycoprotein endopeptidase)
Record Date Created: 19940509

2/9/70

DIALOG(R)File 155:MEDLINE(R)

08167058 94300707 PMID: 8028096

Fatal pneumonia following inoculation of healthy bighorn sheep with Pasteurella haemolytica from healthy domestic sheep.

Foreyt W J; Snipes K P; Kasten R W
Department of Veterinary Microbiology and Pathology, Washington State University, Pullman 99164.

Journal of wildlife diseases (UNITED STATES) Apr 1994, 30 (2) p137-45, ISSN 0090-3558 Journal Code: 0244160
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

In a series of three experiments, isolates of Pasteurella haemolytica biotype A, serotype 2, ribotype reference WSU-1, from healthy domestic

Descriptors: Bacterial Toxins--genetics--GE; *Exotoxins--genetics--GE; * **Pasteurella haemolytica** --genetics--GE; Blotting, Southern; Blotting, Western; Electrophoresis, Gel, Pulsed-Field; Microbial Sensitivity Tests; Mutagenesis; Nitrosoguanidines; Pasteurella haemolytica --growth and development--GD; Restriction Mapping; Selection (Genetics)
CAS Registry No.: 0 (Bacterial Toxins); 0 (Exotoxins); 0 (Nitrosoguanidines); 0 (leukotoxin)
Record Date Created: 19950330

2/9/48
DIALOG(R)File 155:MEDLINE(R)

08965774 96333343 PMID: 8757837
Escherichia coli hemolysin mutants with altered target cell specificity.
Pellett S; Welch R A
Department of Medical Microbiology and Immunology, University of Wisconsin--Madison 53706, USA.
Infection and immunity (UNITED STATES) Aug 1996, 64 (8) p3081-7, ISSN 0019-9567 Journal Code: 0246127
Contract/Grant No.: AI-20323; AI; NIAID
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
In order to understand the functional significance of HlyC-dependent acylation of the Escherichia coli hemolysin structural protein (HlyA), random as well as site-directed substitutions at the known regions of modification, i.e., those at lysine residues at amino acid positions 563 and 689 (HlyAK563 and HlyAK689, respectively), were isolated. Sixteen random hlyA mutations were identified on the basis of a screen for loss of immunoreactivity to the hemolysin-neutralizing D12 monoclonal antibody that reacts to only HlyC-activated HlyA. These substitutions occurred at the region from HlyAE684 to HlyAY696. A recombinant glutathione S-transferase-hemolysin gene fusion encoding glutathione S-transferase-HlyAS608-T725 residues reacts with monoclonal antibody when HlyC is coexpressed with the fusion protein. Therefore, at most only 12% of the total HlyA primary sequence is needed for HlyC-facilitated acylation at the HlyAK689 position, and this modification can occur in the absence of the proximal HlyAK563 acylation site. The cytolytic activities of these HlyA mutants against sheep erythrocytes and bovine and human lymphocyte cell lines (BL-3 and Raji cells, respectively) were analyzed. HlyAK563 and HlyAK689 substitutions displayed various degrees of loss of cytotoxicity that depended on the particular amino acid replacement. An HlyAK563C variant retained greater than 59 and 21% of its BL-3-lytic and erythrolytic activities, respectively, but was nearly inactive against Raji cells. An HlyA mutant with a K-to-E substitution at amino acid 689 (HlyAK689E) was essentially inactive against all three cell types, whereas an HlyAK689R substitution had a pattern of activity similar to that of the HlyAK563C mutant. Preceding the two in vitro acylated HlyA lysines are glycines that appear to be the only amino acids conserved in alignments of these regions among the RTX toxins. Remarkably, considering the retention of cytotoxic activity by some HlYAK689 mutants, each of three different substitutions at the HlyAG688 position was relatively inactive against all three cell types tested. This suggests that HlyAG688 plays a significant structural role in cytotoxic activity apart from its possible participation in an HlyC activation process which presumably requires recognition of pro-HlyA structures. The related RTX toxin, the Pasteurella haemolytica leukotoxin structural protein (LktA), can be activated in an E. coli recombinant background by HlyC. In amino acid sequence alignments, LktAK554 is equivalent to the HlyAK563 position but it has an asparagine (LktAN684) at the homologous HlyAK689 site. An LktAN684K substitution possesses wild-type leukotoxin activity against BL-3 cells and does not acquire hemolytic or Raji cell cytotoxic activity. Surprisingly, both LktAK554C and LktAK554T substitutions retain considerable BL-3 cytotoxicity (45 and 49%,

respectively), indicating that there may be additional lysines within LktA that the HlyC activation mechanism is capable of acylating. Based on these results and a comparison of amino acid sequence alignments of 12 RTX toxins, a putative consensus structure of the RTX residues necessary for HlyC activation is hypothesized.

Tags: Animal; Comparative Study; Human; Support, U.S. Gov't, P.H.S.

Descriptors: *Bacterial Proteins--toxicity--TO; *Bacterial Toxins --toxicity--TO; *Escherichia coli--pathogenicity--PY; *Hemolysins--toxicity --TO; *Mutation; *Protein Processing, Post-Translational; Acylation; Amino Acid Sequence; Bacterial Proteins--genetics--GE; Bacterial Proteins --metabolism--ME; Bacterial Toxins--genetics--GE; Cattle; Dose-Response Relationship, Drug; Escherichia coli--genetics--GE; Exotoxins; Hemolysins --genetics--GE; Hemolysins--metabolism--ME; Hemolysis; Molecular Sequence Data; **Pasteurella haemolytica** --genetics--GE; Pasteurella haemolytica --pathogenicity--PY; Phenotype; Recombinant Fusion Proteins--toxicity--TO; Sequence Homology, Amino Acid; Sheep; Structure-Activity Relationship; Toxicity Tests

CAS Registry No.: 0 (Bacterial Proteins); 0 (Bacterial Toxins); 0 (Exotoxins); 0 (Hemolysins); 0 (Hlya protein); 0 (Recombinant Fusion Proteins); 0 (enterohemorrhagic Escherichia coli-HlyC protein); 0 (leukotoxin)

Record Date Created: 19960926

2/9/21

DIALOG(R)File 155:MEDLINE(R)

10154892 99152574 PMID: 10028248

Taxonomic relationships of the [Pasteurella] haemolytica complex as evaluated by DNA-DNA hybridizations and 16S rRNA sequencing with proposal of Mannheimia haemolytica gen. nov., comb. nov., Mannheimia granulomatis comb. nov., Mannheimia glucosida sp. nov., Mannheimia ruminalis sp. nov. and Mannheimia varigena sp. nov.

Angen O; Mutters R; Caugant D A; Olsen J E; Bisgaard M

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International journal of systematic bacteriology (UNITED STATES) Jan 1999, 49 Pt 1 p67-86, ISSN 0020-7713 Journal Code: 0042143

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The present paper presents the conclusions of a polyphasic investigation of the taxonomy of the trehalose-negative [Pasteurella] haemolytica complex. Clusters previously identified by ribotyping and multilocus enzyme electrophoresis (MEE) have been evaluated by 16S rRNA sequencing and DNA-DNA hybridizations. Results obtained by the different techniques were highly related and indicated that the [P.] haemolytica complex contains distinct genetic and phenotypic groups. At least seven species were outlined, five of which were named. We refrained in formal naming of more groups until additional strains are characterized. Five 16S rRNA clusters were identified corresponding to distinct lineages previously outlined by MEE. Within 16S rRNA cluster I two distinct genotypic groups have been outlined in addition to [P.] haemolytica sensu stricto (biogroup 1). Each of the clusters II, III, IV and V represent at least one new species. The investigations underline that [P.] haemolytica sensu stricto only contains strains that do not ferment L-arabinose even though they are referred to as 'biotype A' of [P.] haemolytica. The five 16S rRNA clusters identified had a common root relative to the other species within the family Pasteurellaceae, and the overall sequence similarity among these five clusters was higher than what is observed within the existing genera of the family. The allocation of the trehalose-negative [P.] haemolytica complex to a new genus seems to be indicated. Based on the polyphasic investigation performed a new genus Mannheimia is proposed for the trehalose-negative [P.] haemolytica complex. At the present stage two previously named species

are transferred to this new genus and three new species are described. [P.] haemolytica is reclassified as Mannheimia haemolytica comb. nov., whereas Pasteurella granulomatis, Bisgaard taxon 20 and [P.] haemolytica biovar 3J are reclassified and combined in the species Mannheimia granulomatis comb. nov. Mannheimia glucosida sp. nov. corresponds to [P.] haemolytica biogroups 3A-3H and the beta-glucosidase and meso-inositol-positive strains of [P.] haemolytica biogroup 9. All typable strains within M. glucosida belong to serotype 11. Mannheimia ruminalis sp. nov. consists of strains previously classified as Bisgaard taxon 18 and [P.] haemolytica biogroup 8D. Finally, Mannheimia varigena sp. nov. includes [P.] haemolytica biogroup 6 as well as Bisgaard taxon 15 and Bisgaard taxon 36. The type strains are NCTC 9380T (M. haemolytica), ATCC 49244T (M. granulomatis), CCUG 38457T = P925T (M. glucosida), CCUG 38470T = HPA92T (M. ruminalis) and CCUG 38462T = 177T (M. varigena).

Tags: Support, Non-U.S. Gov't

Descriptors: *DNA, Bacterial--analysis--AN; *Nucleic Acid Hybridization; *Pasteurella haemolytica--classification--CL; *RNA, Ribosomal, 16S --chemistry--CH; Base Composition; Base Sequence; **Pasteurella haemolytica** --genetics--GE; Phylogeny

Molecular Sequence Databank No.: GENBANK/AF053887; GENBANK/AF053888; GENBANK/AF053889; GENBANK/AF053890; GENBANK/AF053891; GENBANK/AF053892; GENBANK/AF053893; GENBANK/AF053894; GENBANK/AF053895; GENBANK/AF053896; GENBANK/AF053897; GENBANK/AF053898; GENBANK/AF053899; GENBANK/AF053900; GENBANK/AF053901; GENBANK/AF053902; GENBANK/AF060699

CAS Registry No.: 0 (DNA, Bacterial); 0 (RNA, Ribosomal, 16S)

Record Date Created: 19990304

2/9/19

DIALOG(R)File 155:MEDLINE(R)

10282750 99261662 PMID: 10331277

CRITICA: coding region identification tool invoking comparative analysis.

Badger J H; Olsen G J Woese C R U IL, Urbana

Department of Microbiology, University of Illinois, Urbana 61801, USA.

Molecular biology and evolution (UNITED STATES) Apr 1999, 16 (4) p512-24, ISSN 0737-4038 Journal Code: 8501455

Contract/Grant No.: GM07283; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Gene recognition is essential to understanding existing and future DNA sequence data. CRITICA (Coding Region Identification Tool Invoking Comparative Analysis) is a suite of programs for identifying likely protein-coding sequences in DNA by combining comparative analysis of DNA sequences with more common noncomparative methods. In the comparative component of the analysis, regions of DNA are aligned with related sequences from the DNA databases; if the translation of the aligned sequences has greater amino acid identity than expected for the observed percentage nucleotide identity, this is interpreted as evidence for coding. CRITICA also incorporates noncomparative information derived from the relative frequencies of hexanucleotides in coding frames versus other contexts (i.e., dicodon bias). The dicodon usage information is derived by iterative analysis of the data, such that CRITICA is not dependent on the existence or accuracy of coding sequence annotations in the databases. This independence makes the method particularly well suited for the analysis of novel genomes. CRITICA was tested by analyzing the available Salmonella typhimurium DNA sequences. Its predictions were compared with the DNA sequence annotations and with the predictions of GenMark. CRITICA proved to be more accurate than GenMark, and moreover, many of its predictions that would seem to be errors instead reflect problems in the sequence databases. The source code of CRITICA is freely available by anonymous FTP (rdp.life.uiuc.edu in/pub/critica) and on the World Wide Web (http://(/)rdpwww.life.uiuc.edu).

Tags: Comparative Study; Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.

Descriptors: *Sequence Analysis, DNA--methods--MT; *Software; Algorithms; Base Sequence; Codon--genetics--GE; DNA, Bacterial--genetics--GE; Databases, Factual; Evaluation Studies; **Pasteurella haemolytica** --genetics --GE; Salmonella typhimurium--genetics--GE; Sequence Analysis, DNA --statistics and numerical data--SN

CAS Registry No.: 0 (Codon); 0 (DNA, Bacterial)

Identifiers: NASA Discipline Exobiology; Non-NASA Center

Record Date Created: 19990622

2/9/17

DIALOG(R)File 155:MEDLINE(R)

10496975 20031092 PMID: 10566816

Use of a polymerase chain reaction method to detect the leukotoxin gene lktA in biogroup and biovariant isolates of Pasteurella haemolytica and P trehalosi.

Fisher M A; Weiser G C; Hunter D L; Ward A C

Graduate Division of Biological and Biomedical Sciences, Emory University, Atlanta, Georgia 30322, USA.

American journal of veterinary research (UNITED STATES) Nov 1999, 60 (11) p1402-6, ISSN 0002-9645 Journal Code: 0375011

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

OBJECTIVE: To determine whether Pasteurella haemolytica and P trehalosi isolates possess the structural gene for Pasteurella leukotoxin lktA and whether beta-hemolytic activity of these isolates correlated with detection of the lktA gene. SAMPLE POPULATION: 147 P haemolytica isolates from 21 biovariant groups and 101 P trehalosi isolates from 7 biovariant groups. In addition, P multocida and organisms from 7 other genera were tested to establish specificity of the procedure. PROCEDURE: Isolates were observed for beta-hemolysis. A polymerase chain reaction (PCR) procedure was used to amplify the RTX domain of the Pasteurella lktA gene. RESULTS: The lktA gene was detected in 108 (44%) isolates, including 15 associated with respiratory tract disease. All but 2 (98%) of the isolates that had the lktA gene were beta-hemolytic when grown on sheep blood agar. The remaining 140 isolates were negative for the lktA gene and hemolytic activity. CONCLUSIONS AND CLINICAL RELEVANCE: Hemolytic activity of P haemolytica and P trehalosi isolates correlated with detection of the lktA gene for all but 2 isolates. However, 56% of isolates tested were negative for the lktA gene and beta-hemolytic activity. Leukotoxin production and secretion is a major virulence factor when other conditions are favorable for disease development. Therefore, identification of strains that possess the lktA gene may aid in the evaluation of the pathogenic potential of Pasteurella strains carried by wild and domestic animals.

Tags: Animal

Descriptors: *Exotoxins--genetics--GE; *Hemolysins--genetics--GE; *Pasteurella--classification--CL; *Pasteurella Infections--veterinary--VE; *Pasteurella haemolytica--classification--CL; Cattle; Cattle Diseases --diagnosis--DI; Deer; Goat Diseases--diagnosis--DI; Goats; Pasteurella --genetics--GE; Pasteurella--isolation and purification--IP; Pasteurella Infections--diagnosis--DI; **Pasteurella haemolytica** --genetics--GE; Pasteurella haemolytica--isolation and purification--IP; Polymerase Chain Reaction--methods--MT; Sheep; Sheep Diseases--diagnosis--DI; Species Specificity

CAS Registry No.: 0 (Exotoxins); 0 (Hemolysins); 0 (leukotoxin A)

Record Date Created: 20000111

2/9/14

DIALOG(R)File 155:MEDLINE(R)

10776076 20316014 PMID: 10858203

Inactivation of Pasteurella (Mannheimia) haemolytica leukotoxin causes partial attenuation of virulence in a calf challenge model.

Highlander S K; Fedorova N D; Dusek D M; Panciera R; Alvarez L E; Rinehart C

Department of Molecular Virology and Microbiology, Baylor College of Medicine, Houston, Texas 77030, USA. sarahh@bcm.tmc.edu

Infection and immunity (UNITED STATES) Jul 2000, 68 (7) p3916-22, ISSN 0019-9567 Journal Code: 0246127

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The leukotoxin of Pasteurella (Mannheimia) haemolytica is believed to play a significant role in pathogenesis, causing cell lysis and apoptosis that lead to the lung pathology characteristic of bovine shipping fever. Using a system for Cre-lox recombination, a nonpolar mutation within the lktC transacylase gene of the leukotoxin operon was created. The lktC locus was insertionally inactivated using a loxP-aph3-loxP cassette, and then the aph3 marker was excised from the chromosome by Cre recombinase expressed from a P. haemolytica plasmid. The resulting lktC strain (SH2099) secretes inactive leukotoxin and carries no known antibiotic resistance genes. Strain SH2099 was tested for virulence in a calf challenge model. We inoculated 3 x 10(8) or 3 x 10(9) CFU of wild-type or mutant bacteria into the lungs of healthy, colostrum-deprived calves via transthoracic injection. Animals were observed for clinical signs and for nasal colonization for 4 days, after which they were euthanized and necropsied. The lower inoculum (3 x 10(8) CFU) caused significantly fewer deaths and allowed lung pathology to be scored and compared, while the 3 x 10(9) CFU dose of either the wild-type or mutant was lethal to >/=50% of the calves. The estimated 50% lethal dose of SH2099 was four times higher than that of the wild-type strain. Lung lesion scores were reduced twofold in animals inoculated with the mutant, while clinical scores were nearly equivalent for both strains. The wild-type and mutant strains were equally capable of colonizing the upper respiratory tracts of the calves. In this study, the P. haemolytica lktC mutant was shown to be less virulent than the parent strain.

Tags: Animal; Female; Male; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Exotoxins--immunology--IM; *Pasteurella haemolytica --immunology--IM; *Pasteurella haemolytica--pathogenicity--PY; Base Sequence; Cattle; DNA Primers--genetics--GE; Drug Resistance, Microbial --genetics--GE; Exotoxins--genetics--GE; Genes, Bacterial; Models, Biological; Mutation; **Pasteurella haemolytica** --genetics--GE; Pasteurellosis, Pneumonic--immunology--IM; Pasteurellosis, Pneumonic --microbiology--MI; Virulence--genetics--GE; Virulence--immunology--IM

CAS Registry No.: 0 (DNA Primers); 0 (Exotoxins); 0 (leukotoxin)

Record Date Created: 20000720

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$5.25 25 Types

$7.02 Estimated cost File155

$0.22 TELNET

$7.24 Estimated cost this search

$7.24 Estimated total session cost 0.553 DialUnits

Status: Signed Off. (1 minutes)

GENBANK/AF314521; GENBANK/AF314522; GENBANK/AF314523; GENBANK/AF314524; GENBANK/AF314525; GENBANK/AF314526
CAS Registry No.: 0 (Bacterial Proteins); 0 (Bacterial Toxins); 0 (Exotoxins); 0 (Hemolysins); 0 (LktB protein); 0 (LktD protein); 0 (leukotoxin); 0 (leukotoxin A)
Record Date Created: 20011219

2/9/5
DIALOG(R)File 155:MEDLINE(R)

12758277 21423641 PMID: 11532607
Molecular genetic analysis of virulence in Mannheimia (pasteurella) haemolytica.
Highlander S K
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Frontiers in bioscience computer file : a journal and virtual library (United States) Sep 1 2001, 6 pD1128-50, ISSN 1093-4715
Journal Code: 9702166
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Mannheimia haemolytica (previously known as Pasteurella haemolytica) is a weakly hemolytic, gram-negative coccobacillus that is an opportunistic pathogen of cattle, sheep and other ruminants. In stressed, immunocompromised animals, the organism causes a fibrinous, necrotic pneumonia, commonly called "shipping fever". In the United States, economic losses due to shipping fever pneumonia surpass the combined cost of all other diseases of cattle. M. haemolytica, which is a member of the family Pasteurelleaceae, includes twelve serotypes (A1, A2, A5-A9, A12-14, A16 and A17) based on capsular antigen typing. Worldwide, serotypes A1 and A2 predominate, though all serotypes can cause disease. Serotype A1 causes pasteurellosis in cattle and has been the subject extensive study, while serotype A2 causes disease in sheep and is less-well characterized. Potential virulence factors of M. haemolytica have been identified and characterized by gene cloning and DNA sequence analysis. These factors include a ruminant-specific leukotoxin, an anti-phagocytic capsule, lipopolysaccharide, iron-regulated outer membrane proteins, lipoproteins, a sialoglycoprotease, a neuraminidase and two potential immunoglobulin proteases. Unlike the well-characterized leukotoxin, little is known about the expression of these other virulence factors. Attempts to dissect the mechanisms of M. haemolytica pathogenesis have been hindered by the lack of a robust genetic system for mutation of the organism, though new tools for genetic manipulation of M. haemolytica have been developed. Expression plasmids and operon fusion plasmids have been created and a series of antibiotic resistance cassettes useful for site-specific recombination have been constructed. It is anticipated that use of these tools for gene expression and mutagenesis, in combination with the soon to be released genomic sequence of a serotype A1 organism, will aid in understanding the molecular mechanisms of pathogenesis of M. haemolytica and will help to drive development of new vaccines to prevent shipping fever. (243 Refs.)
Tags: Animal; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.
Descriptors: **Pasteurella haemolytica** --genetics--GE; *Pasteurella haemolytica--pathogenicity--PY; Pasteurella haemolytica--classification--CL ; Phylogeny; Serotyping; Virulence--genetics--GE
Record Date Created: 20010904

2/9/4
DIALOG(R)File 155:MEDLINE(R)

Subfile: INDEX MEDICUS

In physical mapping, one orders a set of genetic landmarks or a library of cloned fragments of DNA according to their position in the genome. Our approach to physical mapping divides the problem into smaller and easier subproblems by partitioning the probe set into independent parts (probe contigs). For this purpose we introduce a new distance function between probes, the averaged rank distance (ARD) derived from bootstrap resampling of the raw data. The ARD measures the pairwise distances of probes within a contig and smoothes the distances of probes across different contigs. It shows distinct jumps at contig borders. This makes it appropriate for contig selection by clustering. We have designed a physical mapping algorithm that makes use of these observations and seems to be particularly well suited to the delineation of reliable contigs. We evaluated our method on data sets from two physical mapping projects. On data from the recently sequenced bacterium Xylella fastidiosa, the probe contig set produced by the new method was evaluated using the probe order derived from the sequence information. Our approach yielded a basically correct contig set. On this data we also compared our method to an approach which uses the number of supporting clones to determine contigs. Our map is much more accurate. In comparison to a physical map of Pasteurella haemolytica that was computed using simulated annealing, the newly computed map is considerably cleaner. The results of our method have already proven helpful for the design of experiments aimed at further improving the quality of a map.

Tags: Comparative Study

Descriptors: *Algorithms; *Contig Mapping--statistics and numerical data --SN; Cluster Analysis; Computational Biology; DNA, Bacterial--genetics--GE ; Databases, Factual; **Pasteurella haemolytica** --genetics--GE; gamma Proteobacteria--genetics--GE

CAS Registry No.: 0 (DNA, Bacterial)

Record Date Created: 20010301

2/9/12

DIALOG(R)File 155:MEDLINE(R)

11075054 21101823 PMID: 11157953

Sequence diversity and molecular evolution of the leukotoxin (lktA) gene in bovine and ovine strains of Mannheimia (Pasteurella) haemolytica.

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Journal of bacteriology (United States) Feb 2001, 183 (4) p1394-404, ISSN 0021-9193 Journal Code: 2985120R

Contract/Grant No.: AI22144; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The molecular evolution of the leukotoxin structural gene (lktA) of Mannheimia (Pasteurella) haemolytica was investigated by nucleotide sequence comparison of lktA in 31 bovine and ovine strains representing the various evolutionary lineages and serotypes of the species. Eight major allelic variants (1.4 to 15.7% nucleotide divergence) were identified; these have mosaic structures of varying degrees of complexity reflecting a history of horizontal gene transfer and extensive intragenic recombination. The presence of identical alleles in strains of different genetic backgrounds suggests that assortative (entire gene) recombination has also contributed to strain diversification in M. haemolytica. Five allelic variants occur only in ovine strains and consist of recombinant segments derived from as many as four different sources. Four of these alleles consist of DNA (52.8 to 96.7%) derived from the lktA gene of the two related species Mannheimia glucosida and Pasteurella trehalosi, and four contain recombinant segments derived from an allele that is associated exclusively with bovine or bovine-like serotype A2 strains. The two major